


EXHIBIT D

BLAST**Basic Local Alignment Search Tool**

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Blast 2 sequences

CQ918598:Sequence 15 from Patent WO2004096842Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|56208614|emb|CQ918598.1|

gi|56208614|emb|CQ918598.1|

Description

Sequence 15 from Patent WO2004096842.

Molecule type

dna

Query Length

29751

Subject ID

57133

Description

Contig1

Molecule type

nucleic acid

Subject Length

29736

ProgramBLASTN 2.2.23+ [Citation](#)[Reference](#)

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [Taxonomy reports](#)[Search Parameters](#)**Search parameter name Search parameter value**

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

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Params Ungapped Gapped

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

Results Statistics parameter name Results Statistics parameter value

Effective search space	883426950
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Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

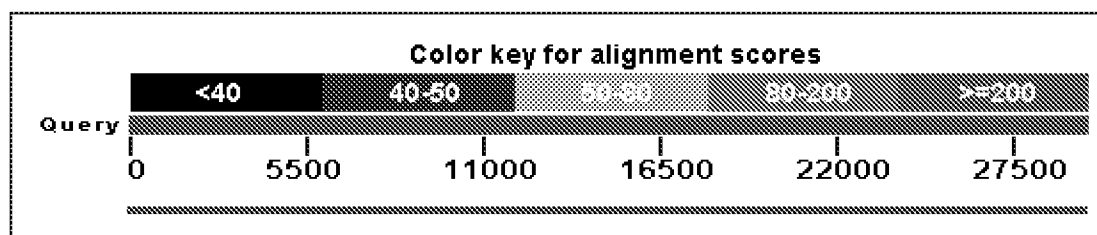


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[Dot Matrix View](#)**Plot of gi|56208614|emb|CQ918598.1| vs 57133 [2]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
57133	Contig1	5.489e+04	5.489e+04	99%	0.0	99%	

Alignments

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

>lcl|57133 Contig1
Length=29736

Score = 5.489e+04 bits (29724), Expect = 0.0
Identities = 29732/29736 (99%), Gaps = 0/29736 (0%)
Strand=Plus/Plus

Query	16	CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAAC TTT	75
Sbjct	1	60
Query	76	AAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAACAATA	135
Sbjct	61	120
Query	136	ATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCTTCTGCAGACTGCTTA	195
Sbjct	121	180
Query	196	CGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTCGTCCGGGTGTGACCG	255
Sbjct	181	240
Query	256	AAAGGTAAGATGGAGAGCCTTGTCTTGGTGTCAACGAGAAAACACACGTCCAAC TCA GT	315
Sbjct	241	300
Query	316	TTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGGGACTCTGTGGAAGAG	375
Sbjct	301	360

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Query	376	GCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAA	435
Sbjct	361	420
Query	436	AAAGGCGTACTGCCCCAGCTTGAACAGCCCTATGTGTTTATTAAACGTTCTGATGCCTTA	495
Sbjct	421	480
Query	496	AGCACCAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATGGACGGCATTTCAGTAC	555
Sbjct	481	540
Query	556	GGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGCGAAACCCCAATTGCA	615
Sbjct	541	600
Query	616	TACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGAGCCGGTGGTCATAGCTATGGC	675
Sbjct	601	660
Query	676	ATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCATTGAAGATTAT	735
Sbjct	661	720
Query	736	GAACAAAAGTGAACACTAAGCATGGCAGTGGTGCCTCCGTGAACCTCACTCGTGAGCTC	795
Sbjct	721	780
Query	796	AATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCAGATGGGTACCCT	855
Sbjct	781	840
Query	856	CTTGATTGCATCAAAGATTTTCTCGCACGCGCGGGCAAGTCAATGTGCACTCTTTCCGAA	915
Sbjct	841	900
Query	916	CAACTTGATTACATCGAGTCGAAGAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAA	975
Sbjct	901	960
Query	976	ATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCTACGAGCACCAGACACCCCTTCGAAATT	1035
Sbjct	961	1020
Query	1036	AAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAGTTTGTGTTTCTCTT	1095
Sbjct	1021	1080
Query	1096	AACTCAAAAGTCAAAGTCATTCAACCACGTGTTGAAAAGAAAAAGACTGAGGGTTTCATG	1155
Sbjct	1081	1140
Query	1156	GGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGAACAATATGCACTTG	1215
Sbjct	1141	1200
Query	1216	TCTACCTTGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAGACGTGCGACTTTCTG	1275
Sbjct	1201	1260
Query	1276	AAAGCCACTTGTGAACATTGTGGCACTGAAAATTTAGTTATTGAAGGACCTACTACATGT	1335
Sbjct	1261	1320
Query	1336	GGGTACCTACCTACTAATGCTGTAGTGAAAATGCCATGTCCTGCCTGTCAAGACCCAGAG	1395
Sbjct	1321	1380
Query	1396	ATTGGACCTGAGCATAGTGTTCAGATTATCACAACCACTCAAACATTGAAACTCGACTC	1455
Sbjct	1381	1440
Query	1456	CGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCCTATGTTGGCTGCTAT	1515
Sbjct	1441	1500
Query	1516	AATAAGCGTGCCTACTGGGTTCCCTCGTGCTAGTGCTGATATTGGCTCAGGCCATACTGGC	1575
Sbjct	1501	1560
Query	1576	ATTACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAA	1635
Sbjct	1561	1620
Query	1636	CGTGTTAACATTAAACATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTG	1695
Sbjct	1621	1680
Query	1696	GCATCTTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAGAGTCTTGATTACAAG	1755
Sbjct	1681	1740
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Sbjct	1741	1800
Query	1816	AAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTTAACACCACTGTGTGGTTTTCCC	1875
Sbjct	1801	1860
Query	1876	TCACAGGCTGCTGGTGTATCAGATCAATTTTTGCGCGCACACTTGATGCAGCAAACCAC	1935
Sbjct	1861	1920
Query	1936	TCAATTCCTGATTGCAAAGAGCAGCTGTCACCATACTTGATGGTATTTCTGAACAGTCA	1995

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Sbjct	1921	1980
Query	1996	TTACGTCTTGTCGACGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGTCAATTATT	2055
Sbjct	1981	2040
Query	2056	ATGGCATATGTAAGTGGTGGTCTTGTACAACAGACTTCTCAGTGGTTGTCTAATCTTTTG	2115
Sbjct	2041	2100
Query	2116	GGCACTACTGTTGAAAACTCAGGCCTATCTTTGAATGGATTGAGGCGAAACTTAGTGCA	2175
Sbjct	2101	2160
Query	2176	GGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATTTCTCATTACAGGTGTTTTT	2235
Sbjct	2161	2220
Query	2236	GACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAGGATTGTGTAAATGC	2295
Sbjct	2221	2280
Query	2296	TTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCGCTGGC	2355
Sbjct	2281	2340
Query	2356	GCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGGACTTTAC	2415
Sbjct	2341	2400
Query	2416	CGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACTACTCATGCCTCTTAAGGCACCAAAA	2475
Sbjct	2401	2460
Query	2476	GAAGTAACCTTTCTTGAAGGTGATTACATGACACAGTACTTACCTCTGAGGAGGTTGTT	2535
Sbjct	2461	2520
Query	2536	CTCAAGAACGGTGAAGTGAAGCACTCGAGACGCCCGTTGATAGCTTCACAAATGGAGCT	2595
Sbjct	2521	2580
Query	2596	ATCGTTGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAGATTAAGGACAAAGAA	2655
Sbjct	2581	2640
Query	2656	CAATACTGCGCATTGTCTCCTGGTTTACTGGCTACAAACAATGTCTTTCGCTTAAAAGGG	2715
Sbjct	2641	2700
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Sbjct	2701	2760
Query	2776	AAGAATGTGAGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAG	2835
Sbjct	2761	2820
Query	2836	TGCTCTGTCTACACTGTTGAATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCA	2895
Sbjct	2821	2880
Query	2896	GAGGCTGTTGTGAAGACTTTACAACCAGTTTCTGATCTCCTTACCAACATGGGTATTGAT	2955
Sbjct	2881	2940
Query	2956	CTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCTGGTGAAGAAAACTTT	3015
Sbjct	2941	3000
Query	3016	TCATCACGTATGTATTGTTCCCTTTTACCCTCCAGATGAGGAAGAAGAGGACGATGCAGAG	3075
Sbjct	3001	3060
Query	3076	TGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTAT	3135
Sbjct	3061	3120
Query	3136	CAAGGTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGAGTTGAGGAAGAAGAA	3195
Sbjct	3121	3180
Query	3196	GAGGAAGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCT	3255
Sbjct	3181	3240
Query	3256	ACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAACTTACTGACAATGTTGCC	3315
Sbjct	3241	3300
Query	3316	ATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTGCTAATCCTATGGTGATTGTAAAT	3375
Sbjct	3301	3360
Query	3376	GCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCACTCAACAAGGCAACC	3435
Sbjct	3361	3420
Query	3436	AATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAATGGCCCTCTTACAGTA	3495
Sbjct	3421	3480
Query	3496	GGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGTCTGCATGTTGTTGGA	3555
Sbjct	3481	3540

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Query	3556	CCTAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAATTTCAAT	3615
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Query	3616	TCACAGGACATCTTACTTGACCATTGTTGTCAGCAGGCATATTTGGTGCTAAACCACTT	3675
Sbjct	3601	3660
Query	3676	CAGTCTTTACAAGTGTGCGTGCAGACGGTTCGTACACAGGTTTATATTGCAGTCAATGAC	3735
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Query	3736	AAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACCTGAAGCCTAGAGTGGAA	3795
Sbjct	3721	3780
Query	3796	GCACCTAAACAAGAGGAGCCACCAAAACACAGAAGATTCCAAAACCTGAGGAGAAATCTGTC	3855
Sbjct	3781	3840
Query	3856	GTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATTGATGAGGTTACCACA	3915
Sbjct	3841	3900
Query	3916	ACACTGGAAGAACTAAGTTTCTTACCAATAAGTTACTCTTGTTTGCTGATATCAATGGT	3975
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Query	3976	AAGCTTTACCATGATTCTCAGAACATGCTTAGAGGTGAAGATATGCTTTTCCTTGAGAAG	4035
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Query	4036	GATGCACCTTACATGGTAGGTGATGTTATCACTAGTGGTGATATCACTTGTGTTGTAATA	4095
Sbjct	4021	4080
Query	4096	CCCTCCAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCTTTGAAGAAAGTGCCA	4155
Sbjct	4081	4140
Query	4156	GTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGTTATACACTTGAGGAA	4215
Sbjct	4141	4200
Query	4216	GCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTACCTTCAGAAGCACCT	4275
Sbjct	4201	4260
Query	4276	AATGCTAAGGAAGAGATTCTAGGAAGTGTATCCTGGAATTTGAGAGAAATGCTTGCTCAT	4335
Sbjct	4261	4320
Query	4336	GCTGAAGAGACAAGAAAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACC	4395
Sbjct	4321	4380
Query	4396	ATCCAACGTAAGTATAAAGGAATTAAATTCAGAGGGCATCGTTGACTATGGTGTCCTGA	4455
Sbjct	4381	4440
Query	4456	TTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACGAAGCTGAACTCTCTA	4515
Sbjct	4441	4500
Query	4516	AATGAGCCGCTTGTACCAATGCCAATTGGTTATGTGACACATGGTTTTAATCTTGAAGAG	4575
Sbjct	4501	4560
Query	4576	GCTGCGCGCTGTATGCGTTCCTTAAAGCTCCTGCCGTAGTGTGAGTATCATCACCAGAT	4635
Sbjct	4561	4620
Query	4636	GCTGTTACTACATATAATGGATACCTCACTTCGTTCATCAAAGACATCTGAGGAGCACTTT	4695
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Query	4696	GTAGAAACAGTTTCTTTGGCTGGCTCTTACAGAGATTGGTCCTATTTCAGGACAGCGTACA	4755
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Query	4756	GAGTTAGGTGTTGAATTTCTTAAAGCGTGGTGACAAAATTGTGTACCACACTCTGGAGAGC	4815
Sbjct	4741	4800
Query	4816	CCCGTCGAGTTTCATCTTGACGGTGAGGTTCTTTCACTTGACAACTAAAGAGTCTCTTA	4875
Sbjct	4801	4860
Query	4876	TCCCTGCGGGAGGTTAAGACTATAAAAGTGTTTCACTGTGGACAACACTAATCTCCAC	4935
Sbjct	4861	4920
Query	4936	ACACAGCTTGTGGATATGTCATGACATATGGACAGCAGTTTGGTCCAACATACTTGGAT	4995
Sbjct	4921	4980
Query	4996	GGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGTAAGACTTTCTTTGTA	5055
Sbjct	4981	5040
Query	5056	CTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTGATGAG	5115
Sbjct	5041	5100

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Query	5116	AGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCACACAAAGAAATGGAAATTTCTCTCAA	5175
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Query	5176	GTTGGTGGTTTAACTTCAATTAAATGGGCTGATAACAATTGTTATTTGTCTAGTGTTTTA	5235
Sbjct	5161	5220
Query	5236	TTAGCACTTCAACAGCTTGAAGTCAAATTCAATGCACCAGCACTTCAAGAGGCTTATTAT	5295
Sbjct	5221	5280
Query	5296	AGAGCCCGTGCTGGTGATGTCTAACTTTTGTGCACTCATACTCGCTTACAGTAATAAA	5355
Sbjct	5281	5340
Query	5356	ACTGTTGGCGAGCTTGGTGATGTCAGAGAACTATGACCCATCTTCTACAGCATGCTAAT	5415
Sbjct	5341	5400
Query	5416	TTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGTGGTCAGAAACTACT	5475
Sbjct	5401	5460
Query	5476	ACCTTAACGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAG	5535
Sbjct	5461	5520
Query	5536	ACAGGTGTTTCCATTCCATGTGTGTGGTCGTGATGCTACACAATATCTAGTACAACAA	5595
Sbjct	5521	5580
Query	5596	GAGTCTTCTTTTGTATGATGTCTGCACCACCTGCTGAGTATAAATTACAGCAAGGTACA	5655
Sbjct	5581	5640
Query	5656	TTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCATTACACTCATATAACT	5715
Sbjct	5641	5700
Query	5716	GCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAGATGTCAGAGTACAAA	5775
Sbjct	5701	5760
Query	5776	GGACCAGTGACTGATGTTTTCTACAAGGAAACATCTTACACTACAACCATCAAGCCTGTG	5835
Sbjct	5761	5820
Query	5836	TCGTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAAATTGGATGGGTATTAT	5895
Sbjct	5821	5880
Query	5896	AAAAAGGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTAACCACTCAACCATTA	5955
Sbjct	5881	5940
Query	5956	CCAAATGCGAGTTTTGATAATTTCAAACCTCACATGTTCTAACACAAAATTTGCTGATGAT	6015
Sbjct	5941	6000
Query	6016	TTAAATCAAATGACAGGCTTCACAAAGCCAGCTTCACGAGAGCTATCTGTCACATTCTTC	6075
Sbjct	6001	6060
Query	6076	CCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTATTCAGCGAGTTTCAAG	6135
Sbjct	6061	6120
Query	6136	AAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACCAAG	6195
Sbjct	6121	6180
Query	6196	ACAACGTTCAAACCAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAGTAGAT	6255
Sbjct	6181	6240
Query	6256	ACTTCAAATTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGAATGGACAATCTTGCT	6315
Sbjct	6241	6300
Query	6316	TGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGTGAAAATCCTACCATACAGAAGGAA	6375
Sbjct	6301	6360
Query	6376	GTCATAGAGTGTGACGTGAAAACCTACCGAAGTTGTAGGCAATGTCATACTTAAACCATCA	6435
Sbjct	6361	6420
Query	6436	GATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGATCTTATGGCTGCTTATGTG	6495
Sbjct	6421	6480
Query	6496	GAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCCTAGCCTTAGGTTTAAAA	6555
Sbjct	6481	6540
Query	6556	ACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGGAGTAAAAATTTGGCT	6615
Sbjct	6541	6600
Query	6616	TATGTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAATTGCGCTAAGAGATTA	6675
Sbjct	6601	6660
Query	6676	GCACAACGTGTGTTTAAACAATTATATGCCTTATGTGTTTACATTATTGTTCCAATTGTGT	6735

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Sbjct	6661	6720
Query	6736	ACTTTTACTAAAAGTACCAATTCTAGAAATTAGAGCTTCACTACCTACAACCTATTGCTAAA	6795
Sbjct	6721	6780
Query	6796	AATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGATGCCGGCATTAAATTATGTGAAGTCA	6855
Sbjct	6781	6840
Query	6856	CCCAAATTTTCTAAATTGTTTCACAATCGCTATGTGGCTATTGTTGTTAAGTATTTGCTTA	6915
Sbjct	6841	6900
Query	6916	GGTTCTCTAATCTGTGTAACCTGCTGCTTTTGGTGTACTCTTATCTAATTTTGGTGCTCCT	6975
Sbjct	6901	6960
Query	6976	TCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAACGTTACTACTATGGAT	7035
Sbjct	6961	7020
Query	7036	TTCTGTGAAGGTTCTTTTCCTTGACGATTTGTTTAAAGTGGATTAGACTCCCTTGATTCT	7095
Sbjct	7021	7080
Query	7096	TATCCAGCTCTTGAAACCATTTCAGGTGACGATTTTCATCGTACAAGCTAGACTTGACAATT	7155
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Query	7156	TTAGGTCTGGCCGCTGAGTGGGTTTGGCATATATGTTGTTTCAAAAATTCTTTTATTTA	7215
Sbjct	7141	7200
Query	7216	TTAGGTCTTTTCACTATAATGCAGGTGTTCTTTGGCTATTTTGCTAGTCATTTTCATCAGC	7275
Sbjct	7201	7260
Query	7276	AATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCACCCGTTTCTGCAATG	7335
Sbjct	7261	7320
Query	7336	GTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTTCATATC	7395
Sbjct	7321	7380
Query	7396	ATGGATGGTTGCACCTCTTCGACTTGCAATGATGTGCTATAAGCGCAATCGTGCCACACGC	7455
Sbjct	7381	7440
Query	7456	GTTGAGTGTACAACCTATTGTTAATGGCATGAAGAGATCTTTCTATGTCTATGCAAATGGA	7515
Sbjct	7441	7500
Query	7516	GGCCGTGGCTTCTGCAAGACTCACAATTGGAATTGTCTCAATTGTGACACATTTTGCCT	7575
Sbjct	7501	7560
Query	7576	GGTAGTACATTTCATTAGTGATGAAGTTGCTCGTGATTGTGCTCACTCCAGTTTAAAAGACCA	7635
Sbjct	7561	7620
Query	7636	ATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTGCTGTGAAAAATGGCGCG	7695
Sbjct	7621	7680
Query	7696	CTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCGCTCTCCCAT	7755
Sbjct	7681	7740
Query	7756	TTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAATGTC	7815
Sbjct	7741	7800
Query	7816	ATAGTTTTTGTATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTGTAC	7875
Sbjct	7801	7860
Query	7876	TACAGTCAGCTGATGTGCCAACCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGACGTT	7935
Sbjct	7861	7920
Query	7936	GGAGATAGTACTGAAGTTTCCGTTAAGATGTTTGATGCTTATGTCGACACCTTTTCAGCA	7995
Sbjct	7921	7980
Query	7996	ACTTTTAGTGTTTCTATGAAAAAATTAAAGGCACTTGTGCTACAGCTCACAGCGAGTTA	8055
Sbjct	7981	8040
Query	8056	GCAAAGGGTGTAGCTTTAGATGGTGTCTTTCTACATTTCGTGTCAGCTGCCCCGACAAGGT	8115
Sbjct	8041	8100
Query	8116	GTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACCTTTCACATCAC	8175
Sbjct	8101	8160
Query	8176	TCTGACTTAGAAGTGACAGGTGACAGTTGTAACAATTTTCATGCTCACCTATAATAAGGTT	8235
Sbjct	8161	8220
Query	8236	GAAAAATGACGCCAGAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAAT	8295
Sbjct	8221	8280

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Query	8296	GCCCAAGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTAAAAGACTACATGTCT	8355
Sbjct	8281	8340
Query	8356	TTATCTGAACAGCTGCGTAAACAAATTCGTAGTGCTGCCAAGAAGAACAACATACCTTTT	8415
Sbjct	8341	8400
Query	8416	AGACTAACTTGTGCTACAAC TAGACAGGTTGTCAATGTCATAACTACTAAAATCTCACTC	8475
Sbjct	8401	8460
Query	8476	AAGGGTGGTAAGATTGTTAGTACTTGTTTTAACTTATGCTTAAGGCCACATTATTGTGC	8535
Sbjct	8461	8520
Query	8536	GTTCTTGCTGCATTGGTTTGTTATATCGTTATGCCAGTACATACATTGTCAATCCATGAT	8595
Sbjct	8521	8580
Query	8596	GGTTACACAAATGAAATCATTGGTTACAAAGCCATT CAGGATGGTGTCACTCGTGACATC	8655
Sbjct	8581	8640
Query	8656	ATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGACGCATGGTTTAGCCAG	8715
Sbjct	8641	8700
Query	8716	CGTGGTGGTTCATACAAAAATGACAAAAGCTGCCCTGTAGTAGCTGCTATCATTACAAGA	8775
Sbjct	8701	8760
Query	8776	GAGATTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAGAGCAATCAATGGTGAC	8835
Sbjct	8761	8820
Query	8836	TTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTGGCAACATTGCTACACACCTTCC	8895
Sbjct	8821	8880
Query	8896	AAACTCATTGAGTATAGTGATTTTGCTACCTCTGCTTGC GTTCTTGCTGCTGAGTGTACA	8955
Sbjct	8881	8940
Query	8956	ATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGACACTAATTTGCTAGAG	9015
Sbjct	8941	9000
Query	9016	GGTTCTATTTCTTATAGTGAGCTTCGTCCAGACACTCGTTATGTGCTTATGGATGGTTCC	9075
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Query	9076	ATCATACAGTTTCCTAACACTTACCTGGAGGGTCTGTTAGAGTAGTAACAAC TTTTGAT	9135
Sbjct	9061	9120
Query	9136	GCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAAGTAGGTATTTGCCTATCTACC	9195
Sbjct	9121	9180
Query	9196	AGTGGTAGATGGGTCTTAATAATGAGCATTACAGAGCTCTATCAGGAGTTTCTGTGGT	9255
Sbjct	9181	9240
Query	9256	GTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTG TGCAACCTGTGGGTGCT	9315
Sbjct	9241	9300
Query	9316	TTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATATTGGTGACTTGTGCT	9375
Sbjct	9301	9360
Query	9376	GCCTACTACTTTATGAAATTCAGACGTGTTTTTGGTGAGTACAACCATGTTGTTGCTGCT	9435
Sbjct	9361	9420
Query	9436	AATGCACTTTTGTTTTTGATGTCTTTCACTATACTCTGTCTGGTACCAGCTTACAGCTTT	9495
Sbjct	9421	9480
Query	9496	CTGCCGGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTATTTACCAATGATGTT	9555
Sbjct	9481	9540
Query	9556	TCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATTGTGCCTTTTGGATA	9615
Sbjct	9541	9600
Query	9616	ACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGGTTCTTTAACAAC TAT	9675
Sbjct	9601	9660
Query	9676	CTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTG	9735
Sbjct	9661	9720
Query	9736	TGTACCTTTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCA	9795
Sbjct	9721	9780
Query	9796	CTTACACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAGTATTT CAGTGAGCC	9855
Sbjct	9781	9840

EXHIBIT D

Query	9856	TTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCAAAGGCTCTAAATGAC	9915
Sbjct	9841	9900
Query	9916	TTTAGCAACTCAGGTGCTGATGTTCTCTACCAACCACCACAGACATCAATCACTTCTGCT	9975
Sbjct	9901	9960
Query	9976	GTTCTGCAGAGTGGTTTTAGGAAAATGGCATTCCCGTCAGGCAAAGTTGAAGGGTGCATG	10035
Sbjct	9961	10020
Query	10036	GTACAAGTAACCTGTGGAACACAACCTCTTAATGGATTGTGGTTGGATGACACAGTATAC	10095
Sbjct	10021	10080
Query	10096	TGTCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCTAACTATGAAGATCTG	10155
Sbjct	10081	10140
Query	10156	CTCATTCGCAAATCCAACCATAGCTTTCTTGTTTCAGGCTGGCAATGTTCAACTTCGTGTT	10215
Sbjct	10141	10200
Query	10216	ATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCTTAAAGTTGATACTTCTAACCCCTAAG	10275
Sbjct	10201	10260
Query	10276	ACACCCAAGTATAAATTTGTCCGTATCCAACCTGGTCAAACATTTTCAGTTCTAGCATGC	10335
Sbjct	10261	10320
Query	10336	TACAATGGTTTACCATCTGGTGTATATCAGTGTGCCATGAGACCTAATCATACCATTAAA	10395
Sbjct	10321	10380
Query	10396	GGTTCTTTCTTAATGGATCATGTGGTAGTGTGGTTTTAACATTGATTATGATTGCGTG	10455
Sbjct	10381	10440
Query	10456	TCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACACGCTGGTACTGACTTA	10515
Sbjct	10441	10500
Query	10516	GAAGGTAAATTCTATGGTCCATTTGTTGACAGACAACTGCACAGGCTGCAGGTACAGAC	10575
Sbjct	10501	10560
Query	10576	ACAACCATAACATTAAATGTTTTGGCATGGCTGTATGCTGCTGTTATCAATGGTGATAGG	10635
Sbjct	10561	10620
Query	10636	TGGTTTCTTAATAGATTCACTACTTTGAATGACTTTAACCTTGTGGCAATGAAGTAC	10695
Sbjct	10621	10680
Query	10696	AACTATGAACCTTTGACACAAGATCATGTTGACATATTGGGACCTCTTTCTGCTCAAACA	10755
Sbjct	10681	10740
Query	10756	GGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTGCAGAATGGTATGAAT	10815
Sbjct	10741	10800
Query	10816	GGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACACCATTGATGTTGTT	10875
Sbjct	10801	10860
Query	10876	AGACAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCAT	10935
Sbjct	10861	10920
Query	10936	CATTGGATGCTTTTAACTTTCTTGACATCACTATTGATTCTTGTTCAAAAGTACACAGTGG	10995
Sbjct	10921	10980
Query	10996	TCACTGTTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTTACTCTTGGTATTATGGCA	11055
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Query	11056	ATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTCTTGCTGTTGTTTCTG	11115
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Sbjct	11101	11160
Query	11176	ATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCTGGTTATAGGCTTAAG	11235
Sbjct	11161	11220
Query	11236	GATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTT	11295
Sbjct	11221	11280
Query	11296	TATGATGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTTACAAA	11355
Sbjct	11281	11340
Query	11356	GTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGCCTTAGTTATTTCTGTA	11415
Sbjct	11341	11400
Query	11416	ACCTCTAACTATTCTGGTGTGCTTACGACTATCATGTTTTTAGCTAGAGCTATAGTGTTT	11475

EXHIBIT D

Sbjct	11401	11460
Query	11476	GTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAACACCTTACAGTGTATCATG	11535
Sbjct	11461	11520
Query	11536	CTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTGTTTACTC	11595
Sbjct	11521	11580
Query	11596	AACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTCTCTACACAAGAATTT	11655
Sbjct	11581	11640
Query	11656	AGGTATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATTGATGCTTTCAAGCTT	11715
Sbjct	11641	11700
Query	11716	AACATTAAGTTGTTGGGTATTGGAGGTAAACCATGTATCAAGTTGCTACTGTACAGTCT	11775
Sbjct	11701	11760
Query	11776	AAAATGTCTGACGTAAAGTGCACATCTGTGGTACTGCTCTCGGTTCTTCAACAACCTAGA	11835
Sbjct	11761	11820
Query	11836	GTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTACAACCTCCACAATGATATTCTTCTT	11895
Sbjct	11821	11880
Query	11896	GCAAAAGACACAACCTGAAGCTTTCGAGAAGATGGTTTCTCTTTTGTCTGTTTGTCTATCC	11955
Sbjct	11881	11940
Query	11956	ATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTCGATAACCGTGCTACT	12015
Sbjct	11941	12000
Query	12016	CTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCC	12075
Sbjct	12001	12060
Query	12076	CAGGAGGCCATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTCGTTCTCAAAAAGTTA	12135
Sbjct	12061	12120
Query	12136	AAGAAATCTTTGAATGTGGCTAAATCTGAGTTTGACCGTGATGCTGCCATGCAACGCAAG	12195
Sbjct	12121	12180
Query	12196	TTGGAAAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAGGCAAGATCTGAGGAC	12255
Sbjct	12181	12240
Query	12256	AAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCACTATGCTTAGGAAGCTT	12315
Sbjct	12241	12300
Query	12316	GATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGTTGTGTTCCACTCAAC	12375
Sbjct	12301	12360
Query	12376	ATCATACCATTGACTACAGCAGCCAAACTCATGGTTGTTGTCCCTGATTATGGTACCTAC	12435
Sbjct	12361	12420
Query	12436	AAGAACACTTGTGATGGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAA	12495
Sbjct	12421	12480
Query	12496	GTTGTTGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATTCACCA	12555
Sbjct	12481	12540
Query	12556	AATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACTCAGCTGTTAAACTACAG	12615
Sbjct	12541	12600
Query	12616	AATAATGAACTGAGTCCAGTAGCACTACGACAGATGTCCGTGTGCGGCTGGTACCACACAA	12675
Sbjct	12601	12660
Query	12676	ACAGCTTGTA CTGATGACAATGCACTTGCC TACTATAACAATTCGAAGGGAGGTAGGTTT	12735
Sbjct	12661	12720
Query	12736	GTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGAT	12795
Sbjct	12721	12780
Query	12796	GGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTTGTACAGACACACCA	12855
Sbjct	12781	12840
Query	12856	AAAGGGCCTAAAGTGAAATACTTGTA CTTCATCAAAGGCTTAAACAACCTAAATAGAGGT	12915
Sbjct	12841	12900
Query	12916	ATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCTTCAGGCTGGAAATGCTACAGAAGTA	12975
Sbjct	12901	12960
Query	12976	CCTGCCAATTCAACTGTGCTTTCCTTCTGTGCTTTTGCAGTAGACCCTGCTAAAGCATAT	13035
Sbjct	12961	13020

EXHIBIT D

Query	13036	AAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGTGAAGATGTTGTGTACA	13095
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Query	13096	CACACTGGTACAGGACAGGCAATTACTGTAAACCAGAAGCTAACATGGACCAAGAGTCC	13155
Sbjct	13081	13140
Query	13156	TTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGACCATCCAAATCCTAAA	13215
Sbjct	13141	13200
Query	13216	GGATTCTGTGACTTGAAAGGTAAGTACGTCCAAATACCTACCACTTGTGCTAATGACCCA	13275
Sbjct	13201	13260
Query	13276	GTGGGTTTTACTTTAGAAACACAGTCTGTACCGTCTGCGGAATGTGGAAAGGTTATGGC	13335
Sbjct	13261	13320
Query	13336	TGTAGTTGTGACCAACTCCGCGAACCCCTTGATGCAGTCTGCGGATGCATCAACGTTTTTA	13395
Sbjct	13321	13380
Query	13396	AACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCACAGGCACTAGTACTG	13455
Sbjct	13381	13440
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Sbjct	13441	13500
Query	13516	TAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCAATTTATTAGACTCTT	13575
Sbjct	13501	13560
Query	13576	ACTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAGAGACTATTTATAACT	13635
Sbjct	13561	13620
Query	13636	TGGTTAAAGATTGTCCAGCGTTGCTGTCCATGACTTTTTCAAGTTTAGAGTAGATGGTG	13695
Sbjct	13621	13680
Query	13696	ACATGGTACCACATATATCACGTCAGCGTCTAACTAAATACACAATGGCTGATTTAGTCT	13755
Sbjct	13681	13740
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Sbjct	13741	13800
Query	13816	ACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATGACTTCGTAGAGAATC	13875
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Sbjct	13921	13980
Query	13996	ATCAGGATCTTAATGGGAAGTGGTACGATTTTCGGTGATTTTCGTACAAGTAGCACCAGGCT	14055
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Sbjct	14221	14280
Query	14296	ATTGTGCAAACCTTTAATGTGTTATTTCTACTGTGTTTCCACCTACAAGTTTGGACCAC	14355
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Query	14356	TAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTGTTTCAACTGGATACCATTTTC	14415
Sbjct	14341	14400
Query	14416	GTGAGTTAGGAGTCGTACATAATCAGGATGTAACTTACATAGCTCGCGTCTCAGTTTCA	14475
Sbjct	14401	14460
Query	14476	AGGAACTTTTAGTGTATGCTGCTGATCCAGCTATGCATGCAGCTTCTGGCAATTTATTGC	14535
Sbjct	14461	14520
Query	14536	TAGATAAACGCACTACATGCTTTTCAGTAGCTGCACTAACAAACAATGTTGCTTTTCAA	14595
Sbjct	14521	14580

EXHIBIT D

Query	14596	CTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGTGTCTAAAGGTTTCT	14655
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Query	14656	TTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTCTTTGCTCAGGATGGCAACGCTG	14715
Sbjct	14641	14700
Query	14716	CTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGTGTGATATCAGACAAC	14775
Sbjct	14701	14760
Query	14776	TCCTATTTCGTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACGATGGTGGCTGTATTA	14835
Sbjct	14761	14820
Query	14836	ATGCCAACCAAGTAATCGTTAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAAT	14895
Sbjct	14821	14880
Query	14896	GGGGTAAGGCTAGACTTTTATTATGACTCAATGAGTTATGAGGATCAAGATGCACCTTTTCG	14955
Sbjct	14881	14940
Query	14956	CGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATCTTAAGTATGCCATTA	15015
Sbjct	14941	15000
Query	15016	GTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTAGTACTATGACAAATA	15075
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Query	15076	GACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAA	15135
Sbjct	15061	15120
Query	15136	TTGGAACAAGCAAGTTTTACGGTGGCTGGCATAATATGTTAAAACTGTTTACAGTGATG	15195
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Query	15196	TAGAAACTCCACACCTTATGGGTTGGGATTATCCAAATGTGACAGAGCCATGCCTAACA	15255
Sbjct	15181	15240
Query	15256	TGCTTAGGATAATGGCCTCTCTTGTCTTGCTCGCAAACATAACACTTGCTGTAACTTAT	15315
Sbjct	15241	15300
Query	15316	CACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAAGTGAGATGGTCATGT	15375
Sbjct	15301	15360
Query	15376	GTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTGATGCTACAACTGCTT	15435
Sbjct	15361	15420
Query	15436	ATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACCTCTTT	15495
Sbjct	15421	15480
Query	15496	CAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCTCTATG	15555
Sbjct	15481	15540
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Sbjct	15541	15600
Query	15616	TGCGTAAACATTTCTCCATGATGATTCTTTCTGATGATGCCGTTGTGTGCTATAACAGTA	15675
Sbjct	15601	15660
Query	15676	ACTATGCGGCTCAAGGTTTAGTAGCTAGCATTAAGAAGTTTAAAGGCAGTTCTTTATTATC	15735
Sbjct	15661	15720
Query	15736	AAAATAATGTGTTTCATGTCTGAGGCAAAATGTTGGACTGAGACTGACCTTACTAAAGGAC	15795
Sbjct	15721	15780
Query	15796	CTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAGATGATTACGTGTACC	15855
Sbjct	15781	15840
Query	15856	TGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTGTCGATGATATTGTCA	15915
Sbjct	15841	15900
Query	15916	AAACAGATGGTACACTTATGATTGAAAGGTTTCGTGTCACCTGGCTATTGATGCTTACCCAC	15975
Sbjct	15901	15960
Query	15976	TTACAAAACATCCTAATCAGGAGTATGCTGATGTCTTTCACTTGTATTTACAATACATTA	16035
Sbjct	15961	16020
Query	16036	GAAAGTTACATGATGAGCTTACTGGCCACATGTTGGACATGTATTCCGTAATGCTAACTA	16095
Sbjct	16021	16080
Query	16096	ATGATAACACCTCACGGTACTGGGAACCTGAGTTTTATGAGGCTATGTACACACCACATA	16155
Sbjct	16081	16140
Query	16156	CAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGACTTCACTTCGTTGCG	16215

EXHIBIT D

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Sbjct	16201	16260
Query	16276	CATCACACAAATTAGTGTGTCTGTTAATCCCTATGTTTGCAATGCCCCAGGTTGTGATG	16335
Sbjct	16261	16320
Query	16336	TCACTGATGTGACACAACGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGC	16395
Sbjct	16321	16380
Query	16396	CTCCCATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTTTATACAAAAACACAT	16455
Sbjct	16381	16440
Query	16456	GTGTAGGCAGTGACAATGTCCTGACTTCAATGCGATAGCAACATGTGATTGGACTAATG	16515
Sbjct	16441	16500
Query	16516	CTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAAGCTTTTCGCAGCAGAAA	16575
Sbjct	16501	16560
Query	16576	CGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTGCCACTGTACGCGAAG	16635
Sbjct	16561	16620
Query	16636	TACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGA	16695
Sbjct	16621	16680
Query	16696	ACAGAAACTATGTCTTTACTGGTTACCGTGTAACATAAAATAGTAAAGTACAGATTGGAG	16755
Sbjct	16681	16740
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Query	16816	ACAAGTTGAATGTTGGTGATTACTTTGTGTTGACATCTCACACTGTAATGCCACTTAGTG	16875
Sbjct	16801	16860
Query	16876	CACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATTACTGGCTTGTACCCAACACTCA	16935
Sbjct	16861	16920
Query	16936	ACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAGGTCGGCATGCAAAGT	16995
Sbjct	16921	16980
Query	16996	ACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACTTGCTC	17055
Sbjct	16981	17040
Query	17056	TCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATGCAGCTGTTGATGCC	17115
Sbjct	17041	17100
Query	17116	TATGTGAAAAGGCATTAAAAATTTGCCCATAGATAAAATGTAGTAGAATCATACCTGCGC	17175
Sbjct	17101	17160
Query	17176	GTGCGCGCGTAGAGTGTTTTGATAAATTCAAAGTGAATTCAACACTAGAACAGTATGTTT	17235
Sbjct	17161	17220
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Sbjct	17221	17280
Query	17296	CTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTCGTGCAAAACACTACG	17355
Sbjct	17281	17340
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Sbjct	17341	17400
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Sbjct	17401	17460
Query	17476	TCCTTGGAACCTGTGCGCGTTGCTGCTGAAATTGTTGACACTGTGAGTGCTTTAGTTT	17535
Sbjct	17461	17520
Query	17536	ATGACAATAAGCTAAAAGCACACAAGGATAAGTCAGCTCAATGCTTCAAAATGTTCTACA	17595
Sbjct	17521	17580
Query	17596	AAGGTGTTATTACACATGATGTTTCATCTGCAATCAACAGACCTCAAATAGGCGTTGTAA	17655
Sbjct	17581	17640
Query	17656	GAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTATCTCACCTTATAATT	17715
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EXHIBIT D

Query	17776	AGGGTTCTGAATATGACTATGTCATATTCACACAACTACTGAAACAGCACACTCTTGTA	17835
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Sbjct	17821	17880
Query	17896	CTGATAGAGATCTTTATGACAACTGCAATTTACAAGTCTAGAAAATACCACGTCGCAATG	17955
Sbjct	17881	17940
Query	17956	TGGCTACATTACAAGCAGAAAAATGTAAGTGGACTTTTTAAGGACTGTAGTAAGATCATT	18015
Sbjct	17941	18000
Query	18016	CTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATATAAAAGTTCAAGACTG	18075
Sbjct	18001	18060
Query	18076	AAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCTACCGTAGACTCATCT	18135
Sbjct	18061	18120
Query	18136	CTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCC	18195
Sbjct	18121	18180
Query	18196	GCGAAGAAGCTATTTCGTACGTTTCGTGCGTGGATTGGCTTTGATGTAGAGGGCTGTCATG	18255
Sbjct	18181	18240
Query	18256	CAACTAGAGATGCTGTGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTA	18315
Sbjct	18241	18300
Query	18316	ACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAG	18375
Sbjct	18301	18360
Query	18376	TTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATACCCTCATGTATAAAG	18435
Sbjct	18361	18420
Query	18436	GCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAAAG	18495
Sbjct	18421	18480
Query	18496	GATTGTCAGACAGAGTCGTGTTTCGTCTTTGGGCGCATGGCTTTGAGCTTACATCAATGA	18555
Sbjct	18481	18540
Query	18556	AGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTT	18615
Sbjct	18541	18600
Query	18616	GCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTGTGGGTTTTGACTATG	18675
Sbjct	18601	18660
Query	18676	TCTATAACCCATTTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAGTA	18735
Sbjct	18661	18720
Query	18736	ACCATGACCAACATTGCCAGGTACATGGAATGCACATGTGGCTAGTTGTGATGCTATCA	18795
Sbjct	18721	18780
Query	18796	TGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAAT	18855
Sbjct	18781	18840
Query	18856	ACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAAGAAAGTACAACACATGG	18915
Sbjct	18841	18900
Query	18916	TTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATTGGAAATCCAA	18975
Sbjct	18901	18960
Query	18976	AGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCAT	19035
Sbjct	18961	19020
Query	19036	GTAGTGACAAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATGCTACACATCACGATA	19095
Sbjct	19021	19080
Query	19096	AATTCAGTATGGTGTGTTTGTGTTTGGAAATTGTAACGTTGATCGTTACCCAGCCAATG	19155
Sbjct	19081	19140
Query	19156	CAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACCTGAACTTACCAGGCTGTGATG	19215
Sbjct	19141	19200
Query	19216	GTGGTAGTTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCAT	19275
Sbjct	19201	19260
Query	19276	TTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATG	19335
Sbjct	19261	19320

EXHIBIT D

Query	19336	GCAACAAGTAGTGTCTGGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACAC	19395
Sbjct	19321	19380
Query	19396	GATGCAATTTAGGTGGTGTCTGTTTGCAGACACCATGCAAATGAGTACCGACAGTACTTGG	19455
Sbjct	19381	19440
Query	19456	ATGCATATAATATGATGATTCTGCTGGATTTAGCCTATGGATTTACAAACAATTTGATA	19515
Sbjct	19441	19500
Query	19516	CTTATAACCTGTGGAATACATTTACCAGGTTACAGAGTTTAGAAAATGTGGCTTATAATG	19575
Sbjct	19501	19560
Query	19576	TTGTTAATAAAGGACACTTTGATGGACACGCCGGCGAAGCACCTGTTTCCATCATTAATA	19635
Sbjct	19561	19620
Query	19636	ATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTGAAAAATAAGACAACAC	19695
Sbjct	19621	19680
Query	19696	TTCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCCAGAGA	19755
Sbjct	19681	19740
Query	19756	TTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTGTAATCTGGGACTACA	19815
Sbjct	19741	19800
Query	19816	AAAGAGAAGCCCCAGCACATGTATCTACAATAGGTGTCTGCACAATGACTGACATTGCCA	19875
Sbjct	19801	19860
Query	19876	AGAAACCTACTGAGAGTGCTTGTCTTCACTTACTGTCTTGTGTTGATGGTAGAGTGGAAG	19935
Sbjct	19861	19920
Query	19936	GACAGGTAGACCTTTTTAGAAACGCCCGTAATGGTGTGTTTAATAACAGAAGGTTCACTCA	19995
Sbjct	19921	19980
Query	19996	AAGGTCTAACACCTTCAAAGGGACCAGCACAAAGCTAGCGTCAATGGAGTCACATTAATTG	20055
Sbjct	19981	20040
Query	20056	GAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACGGCATTATTCAACAGT	20115
Sbjct	20041	20100
Query	20116	TGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTAAGCCCAGATCACAAA	20175
Sbjct	20101	20160
Query	20176	TGGAAACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGCGATATAAGCTCGAGG	20235
Sbjct	20161	20220
Query	20236	GCTATGCCTTCGAACACATCGTTTATGGAGATTTTCAGTCATGGACAACCTTGGCGGTCTTC	20295
Sbjct	20221	20280
Query	20296	ATTTAATGATAGGCTTAGCCAAGCGCTCACAAAGATTCACTTAAATTAGAGGATTTTA	20355
Sbjct	20281	20340
Query	20356	TCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGCAAAACAGGTTTCATCAA	20415
Sbjct	20341	20400
Query	20416	AATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTGCGAGATAATAAAGTCAC	20475
Sbjct	20401	20460
Query	20476	AAGATTTGTCAGTGATTTCAAAGTGGTCAAGGTTACAATTGACTATGCTGAAATTTTCAT	20535
Sbjct	20461	20520
Query	20536	TCATGCTTTGGTGTAAAGGATGGACATGTTGAAACCTTCTACCCAAAACCTACAAGCAAGTC	20595
Sbjct	20521	20580
Query	20596	AAGCGTGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAAGAATGCTTCTTG	20655
Sbjct	20581	G.....	20640
Query	20656	AAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAAAGGAATAATGATGA	20715
Sbjct	20641	20700
Query	20716	ATGTCGCAAAGTATACTCAACTGTGTCAATACTTAAATACACTTACTTTAGCTGTACCCT	20775
Sbjct	20701	20760
Query	20776	ACAACATGAGAGTTATTCACCTTTGGTGCTGGCTCTGATAAAGGAGTTGCACCAGGTACAG	20835
Sbjct	20761	20820
Query	20836	CTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTGATTGAGATCTTAATGACT	20895
Sbjct	20821	20880
Query	20896	TCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATA	20955

EXHIBIT D

Sbjct	20881T.....	20940
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Query	21016	ATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGTGGATTTATAAAGCAAAAAGCTAGCCC	21075
Sbjct	21001	21060
Query	21076	TGGGTGGTTCTATAGCTGTAAAGATAACAGAGCATTCTTGGAATGCTGACCTTTACAAGC	21135
Sbjct	21061	21120
Query	21136	TTATGGGCCATTTCTCATGGTGGACAGCTTTTGTACAAATGTAAATGCATCATCATCGG	21195
Sbjct	21121	21180
Query	21196	AAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAATTGATGGCTATA	21255
Sbjct	21181	21240
Query	21256	CCATGCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCCAGTTGTCTTCCTATT	21315
Sbjct	21241	21300
Query	21316	CACTCTTTGACATGAGCAAATTTCTCTTAAATTAAGAGGAACTGCTGTAATGTCTCTTA	21375
Sbjct	21301	21360
Query	21376	AGGAGAATCAAATCAATGATATGATTTATTCTCTTCTGGAAGGTTAGGCTTATCATT	21435
Sbjct	21361	21420
Query	21436	GAGAAAACAACAGAGTTGTGGTTTCAAGTGATATTCTTGTTAACAACTAAACGAACATGT	21495
Sbjct	21421	21480
Query	21496	TTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCACCACTT	21555
Sbjct	21481	21540
Query	21556	TTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGGGGGGTTTACT	21615
Sbjct	21541	21600
Query	21616	ATCCTGATGAAATTTTATAGATCAGACACTCTTTATTTAACTCAGGATTTATTTCTTCCAT	21675
Sbjct	21601	21660
Query	21676	TTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGCAACCCTGTCATAC	21735
Sbjct	21661	21720
Query	21736	CTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATGTTGTCCGTGGTTGGG	21795
Sbjct	21721	21780
Query	21796	TTTTTGTTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTA	21855
Sbjct	21781	21840
Query	21856	ATGTTGTTATACGAGCATGTAACCTTTGAATTGTGTGACAACCCTTTCTTTGCTGTTTCTA	21915
Sbjct	21841	21900
Query	21916	AACCCATGGGTACACAGACACATACTATGATATTCGATAATGCATTTAATTGCACCTTTCG	21975
Sbjct	21901	21960
Query	21976	AGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAATTTTAAACACT	22035
Sbjct	21961	22020
Query	22036	TACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAAC	22095
Sbjct	22021	22080
Query	22096	CTATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTTTAAGT	22155
Sbjct	22081	22140
Query	22156	TGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTCACCTGCTC	22215
Sbjct	22141	22200
Query	22216	AAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTGGCTATTTAAAGCCAACTACAT	22275
Sbjct	22201	22260
Query	22276	TTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAAAATC	22335
Sbjct	22261	22320
Query	22336	CACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGA	22395
Sbjct	22321	22380
Query	22396	CCTCTAATTTACAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCTAATATTACAACT	22455
Sbjct	22381	22440
Query	22456	TGTGTCCTTTTGGAGAGGTTTTAATGCTACTAAATTCCTTCTGTCTATGCATGGGAGA	22515
Sbjct	22441	22500

EXHIBIT D

Query	22516	GaaaaaaaaTTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACAACCTCAACAttttttt	22575
Sbjct	22501	22560
Query	22576	CAACCTTTTAAGTGCTATGGCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATG	22635
Sbjct	22561	22620
Query	22636	TCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAATAGCGCCAGGACAAA	22695
Sbjct	22621	22680
Query	22696	CTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGATTCATGGGTTGTGTCCTTG	22755
Sbjct	22681	22740
Query	22756	CTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATAAATATAGGT	22815
Sbjct	22741	22800
Query	22816	ATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCC	22875
Sbjct	22801	22860
Query	22876	CTGATGGCAAACCTTGCACCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATG	22935
Sbjct	22861	22920
Query	22936	GTTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTG	22995
Sbjct	22921	22980
Query	22996	AACTTTTAAATGCACCGCCACGGTTTGTGGACCAAATTATCCACTGACCTTATTAAGA	23055
Sbjct	22981	23040
Query	23056	ACCAGTGTGTCAATTTTAAATTTAATGGACTCACTGGTACTGGTGTGTTAACTCCTTCTT	23115
Sbjct	23041	23100
Query	23116	CAAAGAGATTTCAACCATTTCACAATTTGGCCGTGATGTTTCTGATTTCACTGATTCCG	23175
Sbjct	23101	23160
Query	23176	TTCGAGATCCTAAAACATCTGAAATATTAGACATTTACCTTGCGCTTTTGGGGGTGTAA	23235
Sbjct	23161	23220
Query	23236	GTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTA	23295
Sbjct	23221	23280
Query	23296	ACTGCACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATAT	23355
Sbjct	23281	23340
Query	23356	ATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATG	23415
Sbjct	23341	23400
Query	23416	TCGACACTTCTTATGAGTGCACATTCTATTGGAGCTGGCATTGTGCTAGTTACCATA	23475
Sbjct	23401	23460
Query	23476	CAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTTATACTATGTCTTTAG	23535
Sbjct	23461	23520
Query	23536	GTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTTTCAA	23595
Sbjct	23521	23580
Query	23596	TTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATA	23655
Sbjct	23581	23640
Query	23656	TGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTT	23715
Sbjct	23641	23700
Query	23716	GCACACAACCTAAATCGTGCCTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTG	23775
Sbjct	23701	23760
Query	23776	AAGTGTTGCTCAAGTCAAACAAATGTACAAAACCCCACTTTGAAATATTTTGGTGGTT	23835
Sbjct	23761	23820
Query	23836	TTAATTTTTCACAAATATTACCTGACCCTCTAAAGCCAACTAAGAGGTCTTTTATTGAGG	23895
Sbjct	23821	23880
Query	23896	ACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAGCAATATGGCGAAT	23955
Sbjct	23881	23940
Query	23956	GCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTTACAG	24015
Sbjct	23941	24000
Query	24016	TGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTG	24075
Sbjct	24001	24060

EXHIBIT D

Query	24076	GTACTGCCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTA	24135
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Query	24196	AAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAA	24255
Sbjct	24181	24240
Query	24256	CAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAA	24315
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Query	24316	ACACACTTGTTAAACAACCTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATA	24375
Sbjct	24301	24360
Query	24376	TCCTTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCA	24435
Sbjct	24361	24420
Query	24436	GACTTCAAAGCCTTCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATCAGGG	24495
Sbjct	24421	24480
Query	24496	CTTCTGCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGACAATCAAAAAGAG	24555
Sbjct	24481	24540
Query	24556	TTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAGCAGCCCCGCATGGTG	24615
Sbjct	24541	24600
Query	24616	TTGTCTTCCTACATGTCACGTATGTGCCATCCCAGGAGAGGAACTTCACCACAGCGCCAG	24675
Sbjct	24601	24660
Query	24676	CAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTTTGTGTTTAATGGCA	24735
Sbjct	24661	24720
Query	24736	CTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAATTACTACAGACAATA	24795
Sbjct	24721	24780
Query	24796	CATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTATGATC	24855
Sbjct	24781	24840
Query	24856	CTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATA	24915
Sbjct	24841	24900
Query	24916	CATCACCAGATGTTGATCTTGGCGACATTTTCAGGCATTAACGCTTCTGTCGTCAACATTC	24975
Sbjct	24901	24960
Query	24976	AAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACC	25035
Sbjct	24961	25020
Query	25036	TTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTGGTATGTTTGGCTCGGCT	25095
Sbjct	25021	25080
Query	25096	TCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTGTTGCATGACTAGTT	25155
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Query	25156	GTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTTGTTCTTGCTGCAAGTTTGATGAGGATG	25215
Sbjct	25141	25200
Query	25216	ACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACATAAACGAACTTATGGATTT	25275
Sbjct	25201	25260
Query	25276	GTTTATGAGATTTTTTACTCTTAGATCAATTACTGCACAGCCAGTAAAAATTGACAATGC	25335
Sbjct	25261	25320
Query	25336	TTCTCCTGCAAGTACTGTTTCATGCTACAGCAACGATACCGCTACAAGCCTCACTCCCTTT	25395
Sbjct	25321	25380
Query	25396	CGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTCAGAGCGCTACCAAAATAAT	25455
Sbjct	25381	25440
Query	25456	TGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTCATTTGCAATTT	25515
Sbjct	25441	25500
Query	25516	ACTGCTGCTATTTGTTACCATCTATTACATCTTTTGCTTGTCGCTGCAGGTATGGAGGC	25575
Sbjct	25501	25560
Query	25576	GCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCATCAACGCATGTAGAAT	25635
Sbjct	25561	25620
Query	25636	TATTATGAGATGTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCCATTACTTTATGATGC	25695

EXHIBIT D

Sbjct	25621	25680
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Sbjct	25681	25740
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Sbjct	25741	25800
Query	25816	CTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTAAAGACTATGTCGTTGT	25875
Sbjct	25801	25860
Query	25876	ACATGGCTATTTACCGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACAGACAC	25935
Sbjct	25861	25920
Query	25936	TGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGT	25995
Sbjct	25921	25980
Query	25996	GCAAATACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGCAATGGATCCAATTTA	26055
Sbjct	25981	26040
Query	26056	TGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAAGAAAGTGAGTACGAAC	26115
Sbjct	26041	26100
Query	26116	TATGTACTCATTTCGTTTCGGAAGAAACAGGTACGTTAATAGTTAATAGCGTACTTCTTTT	26175
Sbjct	26101	26160
Query	26176	TCTTGCTTTTCGTGGTATTCTTGCTAGTCACACTAGCCATCCTTACTGCGCTTCGATTGTG	26235
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Query	26236	TGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAACGGTTTACGTCTACTC	26295
Sbjct	26221	26280
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Sbjct	26281	26340
Query	26356	ACTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATGGCAGACAACGGTACT	26415
Sbjct	26341	26400
Query	26416	ATTACCGTTGAGGAGCTTAAACAACCTCTGGAACAATGGAACCTAGTAATAGGTTTCCTA	26475
Sbjct	26401	26460
Query	26476	TTCTAGCCTGGATTATGTTACTACAATTTGCCTATTCTAATCGGAACAGGTTTTTG	26535
Sbjct	26461	26520
Query	26536	ATAATAAAGCTTGTTTTCTCTGGCTCTTGTGGCCAGTAACACTTGCTTGTTTTGTGCTT	26595
Sbjct	26521	26580
Query	26596	GCTGCTGTCTACAGAATTAATTGGGTGACTGGCGGATTGCGATTGCAATGGCTTG	26655
Sbjct	26581	26640
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Sbjct	26641	26700
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Sbjct	26701	26760
Query	26776	ATTGTGACCAGACCGCTCATGGAAGTGAACCTGTCATTGGTGCTGTGATCATTCGTGGT	26835
Sbjct	26761	26820
Query	26836	CACTTGCGAATGGCCGGACACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAG	26895
Sbjct	26821	26880
Query	26896	ATCACTGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGAGCGTCGCAGCGTGTA	26955
Sbjct	26881	26940
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Sbjct	26941	27000
Query	27016	ACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTGACAACAGAT	27075
Sbjct	27001	27060
Query	27076	GTTTCATCTTGTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGAC	27135
Sbjct	27061	27120
Query	27136	TTTCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATT	27195
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Query	27196	TAAGCCTCTAACTAAGAAGAATTATTTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGA	27255
Sbjct	27181	27240

EXHIBIT D

Query	27256	TTATCCATAAAACGAACATGAAAAATTATTCTCTTCCTGACATTGATTGTATTTACATCTT	27315
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Sbjct	27301	27360
Query	27376	GCCCATCAGGAACATACGAGGGCAATTCACCATTTACCCTCTTGCTGACAATAAATTTG	27435
Sbjct	27361	27420
Query	27436	CACTAACTTGCTAGCACACACTTTGCTTTTGCTTGCTGACGGTACTCGACATACCT	27495
Sbjct	27421	27480
Query	27496	ATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGACAAGAGGAGGTTCAAC	27555
Sbjct	27481	27540
Query	27556	AAGAGCTCTACTCGCCACTTTTCTCATTGTTGCTGCTCTAGTATTTTAATACTTTGCT	27615
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Query	27616	TCACCATTAAGAGAAAGACAGAATGAATGAGCTCACTTTAATTGACTTCTATTTGTGCTT	27675
Sbjct	27601	27660
Query	27676	TTTAGCCTTTCTGCTATTCCCTGTTTTAATAATGCTTATTATATTTTGGTTTTCACTCGA	27735
Sbjct	27661	27720
Query	27736	AATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGAACATGAACTTCTCATTGT	27795
Sbjct	27721	27780
Query	27796	TTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACAGCGCTGTGCATCTAA	27855
Sbjct	27781	27840
Query	27856	TAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGGGTAATACTTATAGCA	27915
Sbjct	27841	27900
Query	27916	CTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGATGGCACACTATGGTTC	27975
Sbjct	27901	27960
Query	27976	AAACATGCACACCTAATGTTACTATCAACTGTCAAGATCCAGCTGGTGGTGCCTTATAG	28035
Sbjct	27961	28020
Query	28036	CTAGGTGTTGGTACCTTCATGAAGGTACCAAACTGCTGCATTTAGAGACGTACTTGTTG	28095
Sbjct	28021	28080
Query	28096	TTTTAAATAAACGAACAAATTAAAATGTCTGATAATGGACCCCAATCAAACCAACGTAGT	28155
Sbjct	28081	28140
Query	28156	GCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAATAACCAGAATGGAGGA	28215
Sbjct	28141	28200
Query	28216	CGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGTCT	28275
Sbjct	28201	28260
Query	28276	TGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTCCCTCGAGGCCAGGGC	28335
Sbjct	28261	28320
Query	28336	GTTCCAATCAACACCAATAGTGGTCCAGATGACCAAATTGGCTACTACCGAAGAGCTACC	28395
Sbjct	28321	28380
Query	28396	CGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTAT	28455
Sbjct	28381	28440
Query	28456	TACCTAGGAAGTGGCCAGAAGCTTCACTTCCCTACGGCGCTAACAAAGAAGGCATCGTA	28515
Sbjct	28441	28500
Query	28516	TGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCACCCGCAATCCT	28575
Sbjct	28501	28560
Query	28576	AATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACATTGCCAAAAGGCTTC	28635
Sbjct	28561	28620
Query	28636	TACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCCTCATCACGTAGTCGC	28695
Sbjct	28621	28680
Query	28696	GGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCTGCTCGAATGGCT	28755
Sbjct	28681	28740
Query	28756	AGCGGAGGTGGTGAACTGCCCTCGCGCTATTGCTGCTAGACAGATTGAACCAGCTTGAG	28815
Sbjct	28741	28800

EXHIBIT D

Query	28816	AGCAAAGTTTCTGGTAAAGGCCAACAAACAAGGCCAAACTGTCTACTAAGAAATCTGCT	28875
Sbjct	28801	28860
Query	28876	GCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAACAGTACAACGTCACT	28935
Sbjct	28861	28920
Query	28936	CAAGCATTGTTGGGAGACGTGGTCCAGAAACAAACCAAGGAAATTCGGGGACCAAGACCTA	28995
Sbjct	28921	28980
Query	28996	ATCAGACAAGGAACCTGATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAAGTGCC	29055
Sbjct	28981	29040
Query	29056	TCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTG	29115
Sbjct	29041	29100
Query	29116	ACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATA	29175
Sbjct	29101	29160
Query	29176	CTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGCCTaaaaaggac	29235
Sbjct	29161	29220
Query	29236	aaaaagaaaaaGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAAAAGAAGCAGCCCACT	29295
Sbjct	29221	29280
Query	29296	GTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAACTTCAAAATTCCATG	29355
Sbjct	29281	29340
Query	29356	AGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAAGGCAGA	29415
Sbjct	29341	29400
Query	29416	TGGGCTATGTAAACGTTTTTCGCAATTCCGTTTACGATACATAGTCTACTCTTGTGCAGAA	29475
Sbjct	29401	29460
Query	29476	TGAATTCTCGTAACTAAACAGCACAAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAAT	29535
Sbjct	29461	29520
Query	29536	CTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGC	29595
Sbjct	29521	29580
Query	29596	CACGCGGAGTACGATCGAGGCTACAGTGAATAATGCTAGGGAGAGCTGCCTATATGGAAG	29655
Sbjct	29581	29640
Query	29656	AGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTGATTTTAATAGCTTCT	29715
Sbjct	29641	29700
Query	29716	TAGGAGAATGACaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	29751
Sbjct	29701	29736

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